

WEST

☐ ☐ Generate Collection ☐ Print

L7: Entry 1 of 3

File: USPT

Sep 17, 2002

DOCUMENT-IDENTIFIER: US 6451323 B1

TITLE: Recombinant newcastle disease virus RNA expression systems and vaccines

INVENTOR (2):Palese; PeterInventor Group (2):Palese; Peter Leonia NJBrief Summary Text (7):

By contrast, the negative-strand RNA virus, would be attractive candidates for constructing chimeric viruses for use in vaccines. The negative-strand RNA virus, influenza, for example is desirable because its wide genetic variability allows for the construction of a vast repertoire of vaccine formulations which stimulate immunity without risk of developing a tolerance. Recently, construction of infectious recombinant or chimeric negative-strand RNA particles was achieved with the influenza virus (U.S. Pat. No. 5,166,057 to Palese et al., incorporated herein by reference in its entirety).

Brief Summary Text (20):

The negative-sense RNA viruses have been refractory to study of the sequence requirements of the replicase. The purified polymerase of vesicular stomatitis virus is only active in transcription when virus-derived ribonucleoprotein complexes (RNPs) are included as template (De and Banerjee, 1985, Biochem. Biophys. Res. Commun. 126: 40-49; Emerson and Yu, 1975, J. Virol. 15: 1348-1356; Naito and Ishihama, 1976, J. Biol. Chem. 251: 4307-4314). With regard to influenza viruses, it was reported that naked RNA purified from virus was used to reconstitute RNPs. The viral nucleocapsid and polymerase proteins were gel-purified and renatured on the viral RNA using thioredoxin (Szewczyk, et al., 1988, Proc. Natl. Acad. Sci. USA, 85: 7907-7911). However, these authors did not show that the activity of the preparation was specific for influenza viral RNA, nor did they analyze the signals which promote transcription.

Brief Summary Text (21):

Only recently has it been possible to recover negative strand RNA viruses using a recombinant reverse genetics approach (U.S. Pat. No. 5,166,057 to Palese et al.). Although this method was originally applied to engineer influenza viral genomes (Luytjes et al. 1989, Cell 59: 1107-1113; Enami et al. 1990, Proc. Natl. Acad. Sci. USA 87: 11563-11567), it has been successfully applied to a wide variety of segmented and nonsegmented negative strand RNA viruses, including rabies (Schnell et al. 1994, EMBO J. 13:4195-4203); respiratory syncytial virus (Collins et al. 1991, Proc. Natl. Acad. Sci. USA 88:9663-9667); and Sendai virus (Park et al. 1991, Proc. Natl. Acad. Sci. USA 88:5537-5541; Kato et al., 1996, Genes Cells 1:569-579). However, this approach has yet to be applied to Newcastle disease virus RNA genomes.

Brief Summary Text (30):

As used herein, the following terms will have the meanings indicated:  
cRNA=anti-genomic RNA HIV=human immunodeficiency virus L=large protein M=matrix protein (lines inside of envelope) MDCK=Madin Darby canine kidney cells MDBK=Madin Darby bovine kidney cells moi=multiplicity of infection NA=neuraminidase (envelope glycoprotein) NDV=Newcastle disease Virus NP=nucleoprotein (associated with RNA and required for polymerase activity) NS=nonstructural protein (function unknown)